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TECH CENTER 1600/2900



1600

## RAW SEQUENCE LISTING

DATE: 07/29/2003

PATENT APPLICATION: US/09/915,706B

TIME: 11:32:12

Input Set : A:\5112b.app

Output Set: N:\CRF4\07292003\I915706B.raw

3 <110> APPLICANT: NELSON, DAVID R.  
 5 <120> TITLE OF INVENTION: A LIVE, AVIRULENT STRAIN OF V. ANGUILLARUM THAT PROTECTS  
 6 FISH AGAINST INFECTION BY VIRULENT V. ANGUILLARUM AND METHOD  
 7 FOR MAKING THE SAME  
 9 <130> FILE REFERENCE: 5112  
 11 <140> CURRENT APPLICATION NUMBER: 09/915,706B  
 C--> 12 <141> CURRENT FILING DATE: 2003-07-24  
 14 <150> PRIOR APPLICATION NUMBER: 60/220,733  
 15 <151> PRIOR FILING DATE: 2000-07-26  
 17 <160> NUMBER OF SEQ ID NOS: 7  
 19 <170> SOFTWARE: PatentIn Ver. 2.1  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 3588  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Vibrio anguillarum  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: modified\_base  
 28 <222> LOCATION: (3572)  
 29 <223> OTHER INFORMATION: a, t, c, g, other or unknown  
 31 <400> SEQUENCE: 1  
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 34 ccggaaggagg aaaagtgaata atagcttttg agatcagcct gttctagcag cttttcaatg 180  
 35 atcttttttcg tcgttacggt ttgaaaaatc tgacgactgc gtttgtattg caacaagcta 240  
 36 agtggatcca atatctctat ttgataataa aactgctgct tgtctttgct atacctgtg 300  
 37 aattgcagag tgctacatat acctgaaaaa aaacgctttc cagaatctaa ttcgtaagac 360  
 38 acacaaacag ctttacctag gtttttggtg tcgatctcca tgtttgccgc gatggaaacg 420  
 39 gaaaactgac acccgccgga tacgctttcc tctccgatta attgcgtgac aatataactt 480  
 40 ttgctatctg aaagcttaat ggtgaggagg cgggtttggt gctttaattc gttactgctc 540  
 41 atattcaatt aattcactat taaataaaca gttctaaaag gctgtttatt ggatgaatat 600  
 42 tcgaaattat cacataataa ttgatgctat tattacttgc tgtattggtg tcaactttca 660  
 43 tgctctatac atgtaataata tttcgagtta gaccttaatt caaggtaatt tgtctattta 720  
 44 attattatct gaataatatg taatcgattg ctttgtggtt atttttatgt ttgtttcatt 780  
 45 tttaatgacg gtgagcttgt gcattcatat tttttatgat gacaacatct ttgatgaagt 840  
 46 atttaagata ttgttaatgc atgagggggt tgcggtgatt ttttatatta aatcataata 900  
 47 aaatcaacaa tatatgttat tttgtgtctt tttatagtgt tcttttaaaag aggtaggatg 960  
 48 acctaaaggc cgcctaaata tggcgtaaat tgccattgct ataattcacc tcaaagatac 1020  
 49 actattggca aattgacaaa tatgtcactt cgtatgaaac aatattagta gatgttgttt 1080  
 50 ttgctgcaaa aataaaaaatt tttctggttg aaataactca aggcctctag cgttttcctt 1140  
 51 tatcttaaaa tacaggaat agcgattgaa gttaattgac acttaagcaa atagtcaacc 1200  
 52 taacagagca ggaacctatg ctttgttcaa agcatcaaat tgagcaactt tctaaacctc 1260  
 53 tgagtgatga ttcgatctgt ggcgtttatc ttaaaactgga aaaaagtgtt tttcgcccat 1320  
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55 ctgacgagag agatgcgtta caagaggcat gtctaaataa gtggaagatt ctctctgaca 1440
56 gtttgtacga acagttttca aaaacaacca gagatatcga gctcatctca tggtttggtg 1500
57 ctgctcaatt ctttctcgat accacattag aaagtgtctg gaatagcctt gagtgggttag 1560
58 cggatttaag tgagaagcac tgggatcacc tcaaccctgt actaccagtt gaaacgctca 1620
59 aatctgatga tgataagggc aaagaaaagag agcaagcaga tgcgaaaagt aaagcatttt 1680
60 tccaactagt cggcgatagc gaggaaaagt cgatttctta tgcgccggtg ctgcaactgc 1740
61 ccttagtcgg ggaagtgcg ttttttgact ttcaaagtgc agagagaaaa ggcgaaatca 1800
62 gccaaactgaa atctatgctt acgaccacgg tggcgcaaga gcgtttcgca attcaattca 1860
63 agatggaaaa cgccaaacgt tgtgtcacc aattagatcg tttgtcagcg ttggtgagca 1920
64 ctaagtgtca ttctctaggc agtcaaagta ccaacttcgg atttgcaag tctactgctta 1980
65 cccgtgttga aaacgctttg gttcatctaa gtggaattaa gttagcaccg aaagcggagg 2040
66 ccaagacagt agagcaagag gttgccgaaa gttcagtttc tgaaggggag ctgccaaagg 2100
67 atatggatac aaaacatata gagcgaatac cgatggcatc agagcaggct cagaccgtta 2160
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69 acttagcttt ccatttggtg agagaagtct ctgattattt tcgccagagc gaaccgcata 2280
70 gcccaatttc atttttggtt gaaaaagcga ttcgatgggg atatttatcc ttacctgagt 2340
71 tgctgcgaga aatgatgtcg gaacaaaacg gtgacgctct tagtacgatt tttaatgccg 2400
72 ccggttgtaa tcatctcgat caggttttgc tgccggaggt gagtactcca acggtgggca 2460
73 ttgaaagccc ccaaacacct caagcgaagc cttccgtttc ggatccgcga agtggtgaag 2520
74 agcatgtatc tcagacttcc cctgtagata cccaatctaa gcaagatcaa aaaccacaat 2580
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82 ttacaacgtg agcgggactg acggatctca accgtacgag agcctatctc tttcttacac 3060
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85 atgccacgtt aattggcatg tctatttcat gaatatctca ttttaggaca ccgttatggc 3240
86 attgaactca caacataagc gcgttagtaa gaaccgtgtc agcatcacct atgacgttga 3300
87 aacgaatggc gccgtaaaga cgaaagagct gccgtttgtt gttggcgctc ttggcgactt 3360
88 ttcaggacac aaaccagaat cagaaaaagt tgatttagaa gagcgagagt tcacgggtat 3420
89 cgataaagac aacttcgata cagtgatggg gcaaattcac ccgctcttt cgtacaaggt 3480
90 tgataacaag cttgctaata atgatagcca gtttgaagtg aacttgagcc tccgttcgat 3540
W--> 91 gaaagatttc caccagaga acttagttga tnaaattgag ccgcttaa 3588
94 <210> SEQ ID NO: 2
95 <211> LENGTH: 463
96 <212> TYPE: PRT
97 <213> ORGANISM: Vibrio anguillarum
98 <400> SEQUENCE: 2
100 Met Pro Leu Ser Lys His Gln Ile Glu Gln Leu Ser Lys Pro Leu Ser
101 1 5 10 15
103 Asp Asp Ser Ile Cys Gly Val Tyr Leu Lys Leu Glu Lys Ser Ala Phe
104 20 25 30
106 Arg Pro Leu Arg Asn Glu Phe Asn Val Ala Gln Thr Ala Leu Arg Lys
107 35 40 45
109 Leu Ser Gln Asn Pro Ser Ala Asp Glu Arg Asp Ala Leu Gln Glu Ala

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110      50                      55                      60
112 Cys Leu Asn Lys Trp Lys Ile Leu Ser Asp Ser Leu Tyr Glu Gln Phe
113 65                      70                      75                      80
115 Ser Lys Thr Thr Arg Asp Ile Glu Leu Ile Ser Trp Phe Val Ala Ala
116                      85                      90                      95
118 Gln Phe Leu Leu Asp Thr Thr Leu Glu Ser Ala Ala Asn Ser Leu Glu
119                      100                      105                      110
121 Trp Leu Ala Asp Leu Ser Glu Lys His Trp Asp His Leu Asn Pro Val
122                      115                      120                      125
124 Leu Pro Val Glu Thr Leu Lys Ser Asp Asp Asp Lys Gly Lys Glu Arg
125                      130                      135                      140
127 Glu Gln Ala Asp Ala Lys Val Lys Ala Phe Phe Gln Leu Val Gly Asp
128 145                      150                      155                      160
130 Ser Glu Glu Ser Ser Ile Leu Tyr Ala Pro Val Leu Gln Leu Pro Leu
131                      165                      170                      175
133 Val Gly Glu Val Thr Phe Phe Asp Phe Gln Ser Ala Glu Arg Lys Gly
134                      180                      185                      190
136 Glu Ile Ser Gln Leu Lys Ser Met Leu Thr Thr Thr Val Ala Gln Glu
137                      195                      200                      205
139 Arg Phe Ala Ile Gln Phe Lys Met Glu Asn Ala Lys Arg Cys Val Thr
140                      210                      215                      220
142 Gln Leu Asp Arg Leu Ser Ala Leu Val Ser Thr Lys Cys His Ser Leu
143 225                      230                      235                      240
145 Gly Ser Gln Ser Thr Asn Phe Gly Phe Ala Lys Ser Leu Leu Thr Arg
146                      245                      250                      255
148 Val Glu Asn Ala Leu Val His Leu Ser Gly Ile Lys Leu Ala Pro Lys
149                      260                      265                      270
151 Ala Glu Ala Lys Thr Val Glu Gln Glu Val Ala Glu Ser Ser Val Ser
152                      275                      280                      285
154 Glu Gly Glu Leu Pro Ser His Met Asp Thr Lys His Ile Glu Arg Ile
155                      290                      295                      300
157 Pro Met Ala Ser Glu Gln Ala Gln Thr Val Ser Gln His Leu His Ala
158 305                      310                      315                      320
160 Gly Asn Leu Ser Glu Leu Gly Asn Leu Asn Asn Met Asn Arg Asp Leu
161                      325                      330                      335
163 Ala Phe His Leu Leu Arg Glu Val Ser Asp Tyr Phe Arg Gln Ser Glu
164                      340                      345                      350
166 Pro His Ser Pro Ile Ser Phe Leu Leu Glu Lys Ala Ile Arg Trp Gly
167                      355                      360                      365
169 Tyr Leu Ser Leu Pro Glu Leu Leu Arg Glu Met Met Ser Glu Gln Asn
170                      370                      375                      380
172 Gly Asp Ala Leu Ser Thr Ile Phe Asn Ala Ala Gly Leu Asn His Leu
173 385                      390                      395                      400
175 Asp Gln Val Leu Leu Pro Glu Val Ser Thr Pro Thr Val Gly Ile Glu
176                      405                      410                      415
178 Ser Pro Gln Thr Pro Gln Ala Lys Pro Ser Val Ser Asp Pro Arg Ser
179                      420                      425                      430
181 Val Glu Glu His Val Ser Gln Thr Ser Pro Val Asp Thr Gln Ser Lys
182                      435                      440                      445

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184 Gln Asp Gln Lys Pro Gln Ser Ser Ala Thr Ser Ala Leu Ser Trp
185      450                      455                      460
188 <210> SEQ ID NO: 3
189 <211> LENGTH: 176
190 <212> TYPE: PRT
191 <213> ORGANISM: Vibrio anguillarum
193 <400> SEQUENCE: 3
194 Met Ala Ser Ile Tyr Met Arg Val Ser Gly Leu Gln Val Glu Gly Ala
195 1      5      10      15
197 Ala Thr Ile Gly Gln Leu Glu Thr Ala Glu Gly Lys Asn Asp Gly Trp
198      20      25      30
200 Phe Ala Ile Asn Ser Tyr Ser Trp Gly Gly Ala Arg Asn Val Ala Met
201      35      40      45
203 Asp Ile Gly Asn Gly Thr Asn Ala Asp Ser Gly Met Val Gly Val Ser
204      50      55      60
206 Glu Val Ser Val Thr Lys Glu Val Asp Gly Ala Ser Glu Asp Leu Leu
207 65      70      75      80
209 Ser Tyr Leu Phe Asn Pro Gly Lys Asp Gly Lys Thr Val Glu Val Ala
210      85      90      95
212 Phe Thr Lys Pro Ser Asn Asp Gly Gln Gly Ala Asp Val Tyr Phe Gln
213      100     105     110
215 Val Lys Leu Glu Lys Ala Arg Leu Val Ser Tyr Asn Val Ser Gly Thr
216      115     120     125
218 Asp Gly Ser Gln Pro Tyr Glu Ser Leu Ser Leu Ser Tyr Thr Ser Ile
219      130     135     140
221 Ser Gln Lys His His Tyr Glu Lys Glu Gly Glu Glu Leu Gln Ser Gly
222 145     150     155     160
224 Gly Val Val Thr Tyr Asp Leu Pro Thr Gly Lys Met Thr Ser Gly Lys
225      165     170     175
227 <210> SEQ ID NO: 4
228 <211> LENGTH: 117
229 <212> TYPE: PRT
230 <213> ORGANISM: Vibrio anguillarum
232 <220> FEATURE:
233 <221> NAME/KEY: MOD_RES
234 <222> LOCATION: (113)
235 <223> OTHER INFORMATION: Variable amino acid
237 <400> SEQUENCE: 4
238 Met Ala Leu Asn Ser Gln His Lys Arg Val Ser Lys Asn Arg Val Ser
239 1      5      10      15
241 Ile Thr Tyr Asp Val Glu Thr Asn Gly Ala Val Lys Thr Lys Glu Leu
242      20      25      30
244 Pro Phe Val Val Gly Val Ile Gly Asp Phe Ser Gly His Lys Pro Glu
245      35      40      45
247 Ser Glu Lys Val Asp Leu Glu Arg Glu Phe Thr Gly Ile Asp Lys
248      50      55      60
250 Asp Asn Phe Asp Thr Val Met Gly Gln Ile His Pro Arg Leu Ser Tyr
251 65      70      75      80
253 Lys Val Asp Asn Lys Leu Ala Asn Asp Asp Ser Gln Phe Glu Val Asn

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      254                85                90                95
256 Leu Ser Leu Arg Ser Met Lys Asp Phe His Pro Glu Asn Leu Val Asp
257                100                105                110
W--> 259 Xaa Ile Glu Pro Leu
260                115
263 <210> SEQ ID NO: 5
264 <211> LENGTH: 31
265 <212> TYPE: DNA
266 <213> ORGANISM: Artificial Sequence
268 <220> FEATURE:
269 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
271 <400> SEQUENCE: 5
272 tttctgcagc tggttgaaat aactcaaggc c 31
275 <210> SEQ ID NO: 6
276 <211> LENGTH: 32
277 <212> TYPE: DNA
278 <213> ORGANISM: Artificial Sequence
280 <220> FEATURE:
281 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
283 <400> SEQUENCE: 6
284 tttctgcagg gatccgaaac ggaaggcttc gc 32
287 <210> SEQ ID NO: 7
288 <211> LENGTH: 29
289 <212> TYPE: DNA
290 <213> ORGANISM: Artificial Sequence
292 <220> FEATURE:
293 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
295 <400> SEQUENCE: 7
296 tttaagcttc acgcatgtaa atacttgcc 29

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 3572  
Seq#:4; Xaa Pos. 113